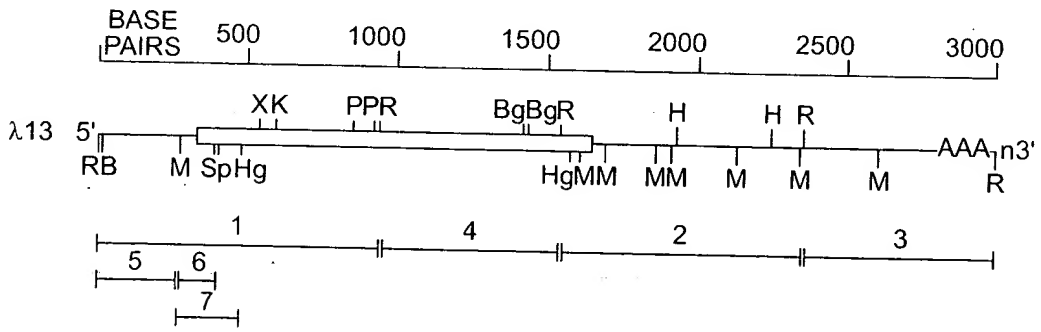

FIG. 1

```
CGGGGTAGGATCCGGAACGCATTCGGAAGGCTTTTTGCAAGCATTTACTTGGAAGGAGAACTTGGGATCTTTCTG      75

GGAACCCCCCGCCCCGGCTGGATTGGCCGAGCAAGCCTGGAAAATGGTAAATGATCATTTGGATCAATTACAGGC     150

TTTTAGCTGGCTTGTCTGTCATAATTCATGATTCGGGGCTGGGAAAAAGACCAACAGCCTACGTGCCAAAAAAGG     225

GGCAGAGTTTGATGGAGTTGGGTGGACTTTTCTATGCCATTTGCCTCCACACCTAGAGGATAAGCACTTTTGCAG     300
                    1                   10
                  MetPheAspCysMetAspValLeuSerValSerProGlyGlnIleLeuAspPhe
ACATTCAGTGCAAGGGAGATCATGTTTGACTGTATGGATGTTCTGTCAGTGAGTCCTGGGCAAATCCTGGATTTC     375
  20                  30                  40
TyrThrAlaSerProSerSerCysMetLeuGlnGluLysAlnLeuLysAlaCysPheSerGlyLeuThrGlnThr
TACACTGCGAGTCCGTCTTCCTGCATGCTCCAGGAGAAAGCTCTCAAAGCATGCTTCAGTGGATTGACCCAAACC     450
          50                  60
GluTrpGlnHisArgHisThrAlaGlnSerIleGluThrGlnSerThrSerSerGluGluLeuValProSerPro
GAATGGCAGCATCGGCACACTGCTCAATCAATTGAAACACAGAGCACCAGCTCTGAGGAACTCGTCCCAAGCCCC     525
  70                  80 ⟶               90
ProSerProLeuProProProArgValTyrLysProCysPheValCysGlnAspLysSerSerGlyTyrHisTyr
CCATCTCCACTTCCTCCCCCTCGAGTGTACAAACCCTGCTTCGTCTGCCAGGACAAATCATCAGGGTACCACTAT     600
              100                 110
GlyValSerAlaCysGluGlyCysLysGlyPhePheArgArgSerIleGlnLysAsnMetIleTyrThrCysHis
GGGGTCAGCGCCTGTGAGGGATGTAAGGGCTTTTTCCGCAGAAGTATTCAGAAGAATATGATTTACACTTGTCAC     675
  120                 130                 140
ArgAspLysAsnCysValIleAsnLysValThrArgAsnArgCysGlnTyrCysArgLeuGlnLysCysPheGlu
CGAGATAAGAACTGTGTTATTAATAAAGTCACCAGGAATCGATGCCAATACTGTCGACTCCAGAAGTGCTTTGAA     750
    ⟵         150                 160
ValGlyMetSerLysGluSerValArgAsnAspArgAsnLysLysLysLysGluThrSerLysGlnGluCysThr
GTGGGAATGTCCAAAGAATCTGTCAGGAATGACAGGAACAAGAAAAAGAAGGAGACTTCGAAGCAAGAATGCACA     825
  170                 180                 190
GluSerTyrGluMetThrAlaGluLeuAspAspLeuThrGluLysIleArgLysAlaHisGlnGluThrPhePro
GAGAGCTATGAAATGACAGCTGAGTTGGACGATCTCACAGAGAAGATCCGAAAAGCTCACCAGGAAACTTTCCCT     900
              200                 210
SerLeuCysGlnLeuGlyLysTyrThrThrAsnSerSerAlaAspHisArgValArgLeuAspLeuGlyLeuTrp
TCACTCTGCCAGCTGGGTAAATACACCACGAATTCCAGTGCTGACCATCGAGTCCGACTGGACCTGGGCCTCTGG     975
  220                 230                 240
AspLysPheSerGluLeuAlaThrLysCysIleIleLysIleValGluPheAlaLysArgLeuProGlyPheThr
GACAAATTCAGTGAACTGGCCACCAAGTGCATTATTAAGATCGTGGAGTTTGCTAAACGTCTGCCTGGTTTCACT    1050
              250                 260
GlyLeuThrIleAlnAspGlnIleThrLeuLeuLysAlaAlaCysLeuAspIleLeuIleLeuArgIleCysThr
GGCTTGACCATCGCAGACCAAATTACCCTGCTGAAGGCCGCCTGCCTGGACATCCTGATTCTTAGAATTTGCACC    1125
```

FIG. 2A

```
ArgTyrThrProGluGlnAspThrMetThrPheSerAspGlyLeuThrLeuAsnArgThrGlnMetHisAsnAla
AGGTATACCCCAGAACAAGACACCATGACTTTCTCAGACGGCCTTACCCTAAATCGAACTCAGATGCACAATGCT   1200
                  300                 310
GlyPheGlyProLeuThrAspLeuValPheThrPheAlaAsnGlnLeuLeuProLeuGluMetAspAspThrGlu
GGATTTGGTCCTCTGACTGACCTTGTGTTCACCTTTGCCAACCAGCTCCTGCCTTTGGAAATGGATGACACAGAA   1275
   320                 330                 340
ThrGlyLeuLeuSerAlaIleCysLeuIleCysGlyAspArgGlnAspLeuGluGluProThrLysValAspLys
ACAGGCCTTCTCAGTGCCATCTGCTTAATCTGTGGAGACCGCCAGGACCTTGAGGAACCGACAAAAGTAGATAAG   1350
                  350                 360
LeuGlnGluProLeuLeuGluAlaLeuLysIleTyrIleArgLysArgArgProSerLysProHisMetPhePro
CTACAAGAACCATTGCTGGAAGCACTAAAAATTTATATCAGAAAAAGACGACCCAGCAAGCCTCACATGTTTCCA   1425
   370                 380                 390
LysIleLeuMetLysIleThrAspLeuArgSerIleSerAlaLysGlyAlaGluArgValIleThrLeuLysMet
AAGATCTTAATGAAAATCACAGATCTCCGTAGCATCAGTGCTAAAGGTGCAGAGCGTGTAATTACCTTGAAAATG   1500
                  400                 410
GluIleProGlySerMetProProLeuIleGlnGluMetMetGluAsnSerGluGlyHisGluProLeuThrPro
GAAATTCCTGGATCAATGCCACCTCTCATTCAAGAAATGATGGAGAATTCTGAAGGACATGAACCCTTGACCCCA   1575
   420                 430                 440
SerSerSerGlyAsnThrAlaGluHisSerProSerIleSerProSerSerValGluAsnSerGlyValSerGln
AGTTCAAGTGGGAACACAGCAGAGCACAGTCCTAGCATCTCACCCAGCTCAGTGGAAAACAGTGGGGTCAGTCAG   1650

SerProLeuValGlnSTOP
TCACCACTCGTGCAATAAGACATTTTCTAGCTACTTCAAACATTCCCCAGTACCTTCAGTTCCAGGATTTAAAAT   1725
GCAAGAAAAAACATTTTTACTGCTGCTTAGTTTTTGGACTGAAAAGATATTAAAACTCAAGAAGGACCAAGAAGT   1800
TTTCATATGTATCAATATATATACTCCTCACTGTGTAACTTACCTAGAAATACAAACTTTTCCAATTTTAAAAAA   1875
TCAGCCATTTCATGCAACCAGAAACTAGTTAAAAGCTTCTATTTTCCTCTTTGAACACTCAAGATGCATGGCAAA   1950
GACCCAGTCAAAATGATTTACCCCTGGTTAAGTTTCTGAAGACTTTGTACATACAGAAGTATGGCTCTGTTCTTT   2025
CTATACTGTATGTTTGGTGCTTTCCTTTTGTCTTGCATACTCAAAATAACCATGACACCAAGGTTATGAAATAGA   2100
CTACTGTACACGTCTACCTAGGTTCAAAAAGATAACTGTCTTGCTTTCATGGAATAGTCAAGACATCAAGGTAAG   2175
GAAACAGGACTATTGACAGGACTATTGTACAGTATGACAAGATAAGGCTGAAGATATTCTACTTTAGTTAGTATG   2250
GAAGCTTGTCTTTGCTCTTTCTGATGCTCTCAAACTGCATCTTTTATTTCATGTTGCCCAGTAAAAGTATACAAA   2325
TTCCCTGCACTAGCAGAAGAGAATTCTGTATCAGTGTAACTGCCAGTTCAGTTAATCAAATGTCATTTGTTCAAT   2400
TGTTAATGTCACTTTAAATTAAAAGTGGTTTATTACTTGTTTAATGACATAACTACACAGTTAGTTAAAAAAAAT   2475
TTTTTTACAGTAATGATAGCCTCCAAGGCAGAAACACTTTTCAGTGTTAAGTTTTTGTTTACTTGTTCACAAGCC   2550
ATTAGGGAAATTTCATGGGATAATTAGCAGGCTGGTCTACCACTGGACCATGTAACTCTAGTGTCCTTCCTGATT   2625
CATGCCTGATATTGGGATTTTTTTCCAGCCCTTCTTGATGCCAAGGGCTAATTATATTACATCCCAAAGAAACAG   2700
GCATAGAATCTGCCTCCTTTGACCTTGTTCAATCACTATGAAGCAGAGTGAAAGCTGTGGTAGAGTGGTTAACAG   2775
ATACAAGTGTCAGTTTCTTAGTTCTCATTTAAGCACTAGTGGAATTTTTTTTTTTGATATATTAGCAAGTCTGTG   2850
ATGTACTTTCACTGGCTCTGTTTGTACATTGAGATTGTTTGTTTAACAATGCTTTCTATGTTCATATACTGTTTA   2925
CCTTTTTCCATGGAGTCTCCTGGCAAAGAATAAAATATATTTATTTTAAAAAAAAAAAAAAAAAAAA           2992
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FIG. 2B

FIG. 3

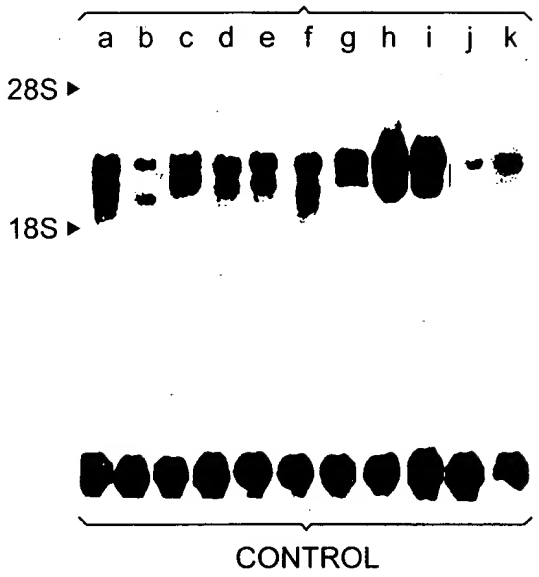


FIG. 4

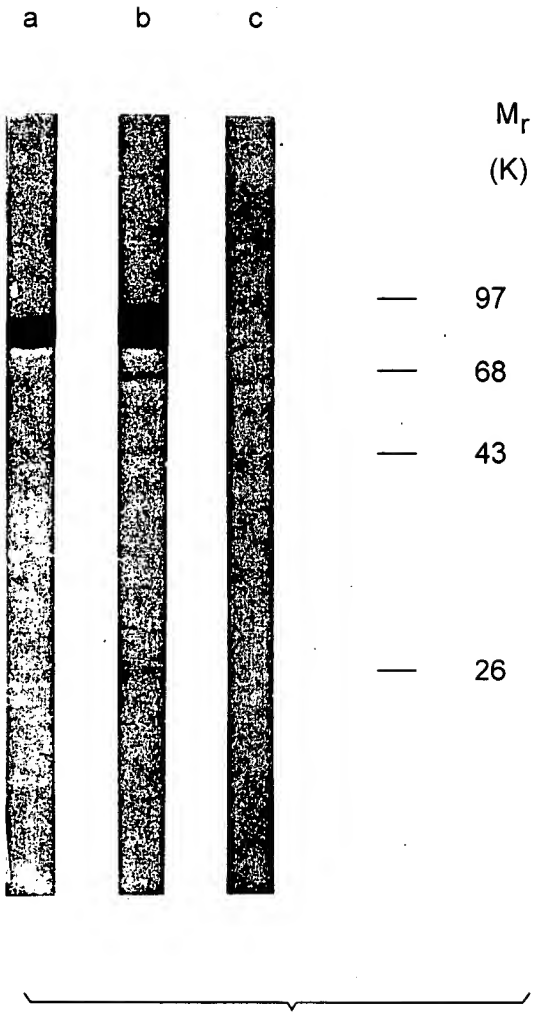


FIG. 5

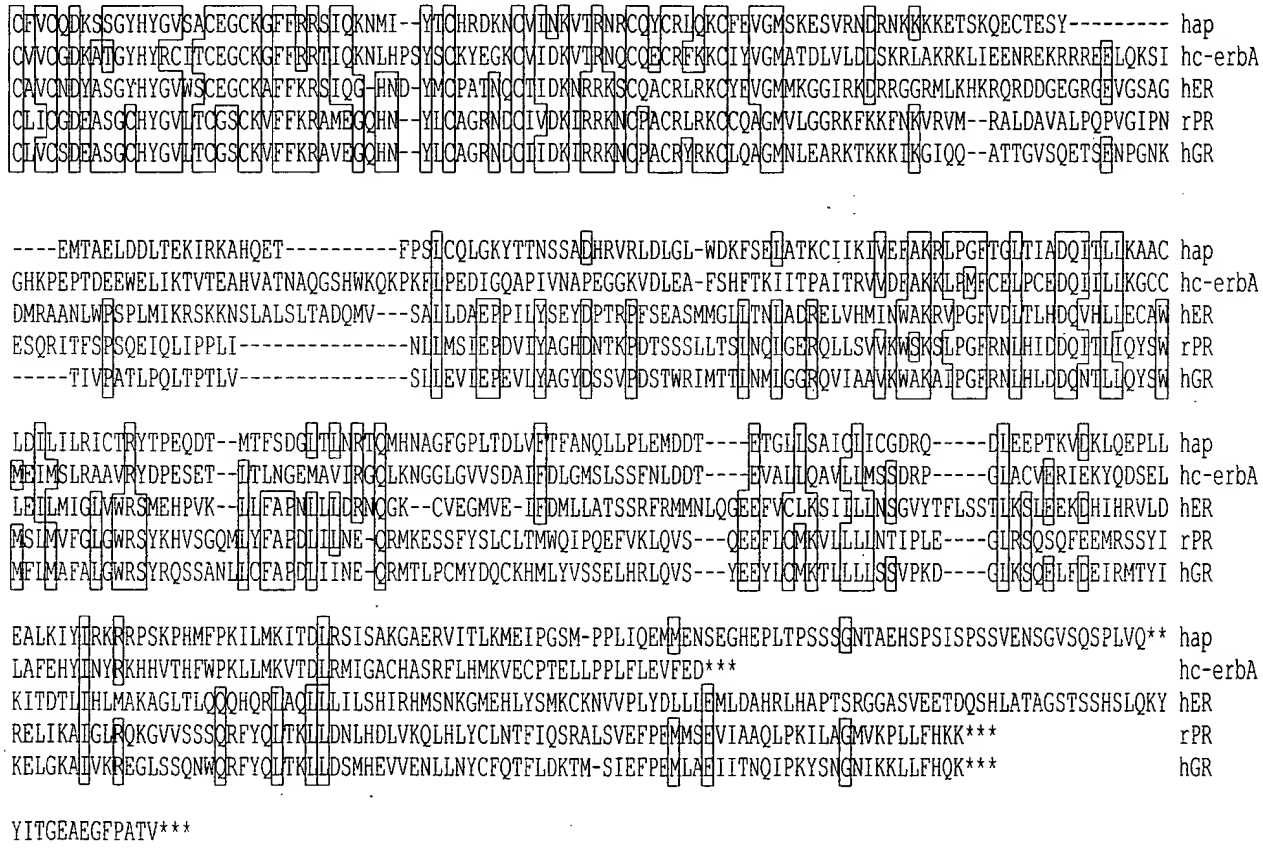


FIG. 6

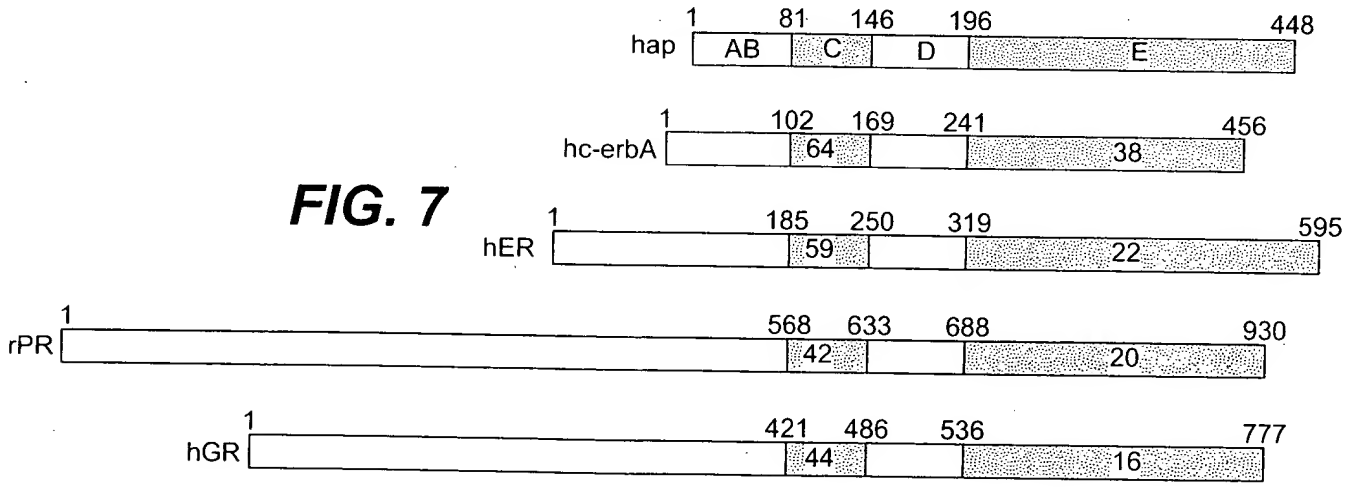


FIG. 7

FIG. 8C

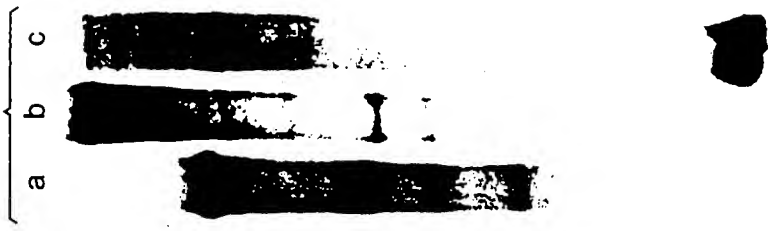


FIG. 8B

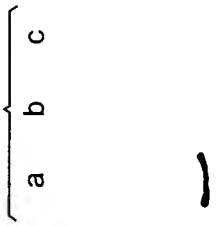
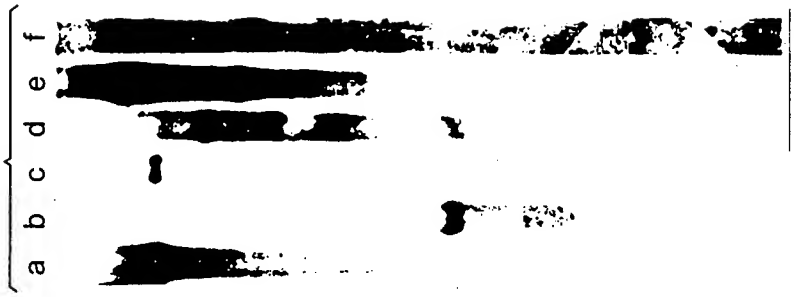


FIG. 8A



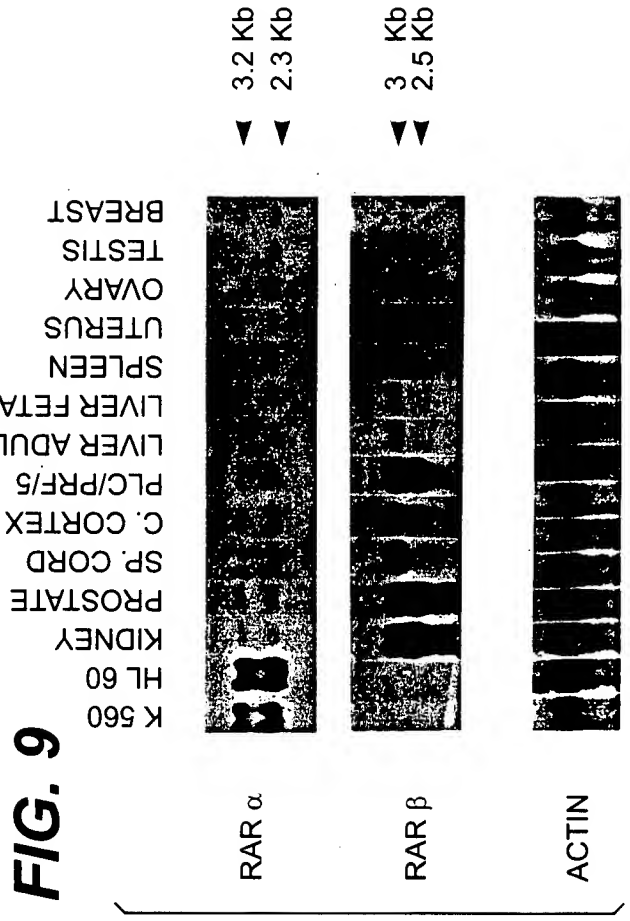
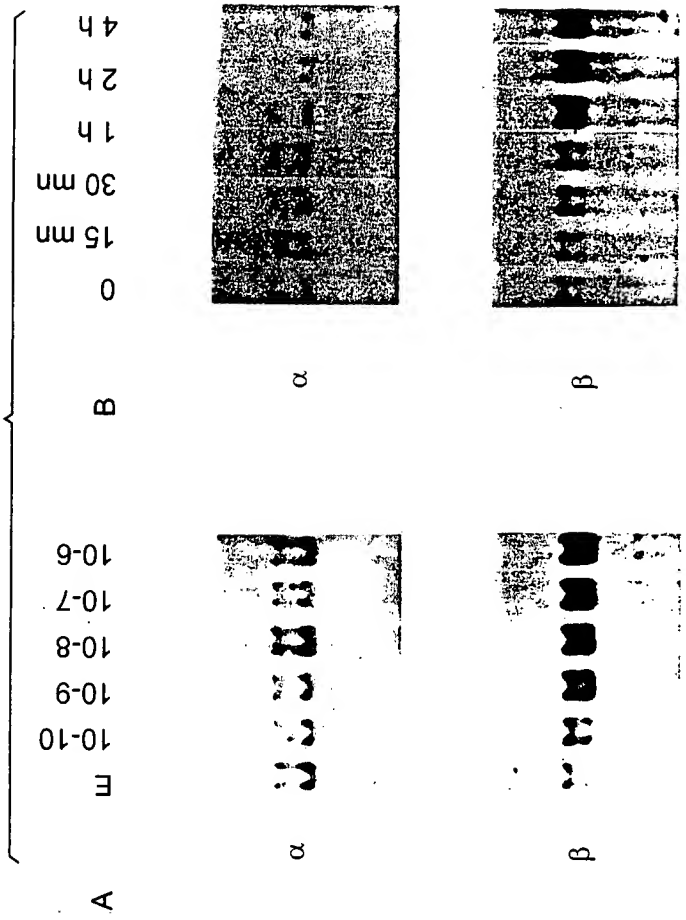


FIG. 9

FIG. 10



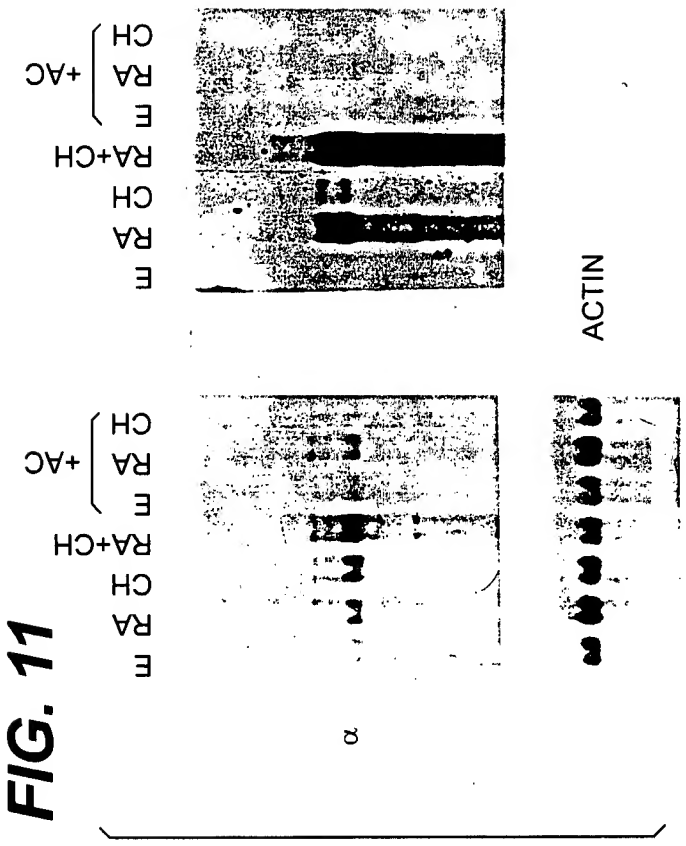


FIG. 11

FIG. 12

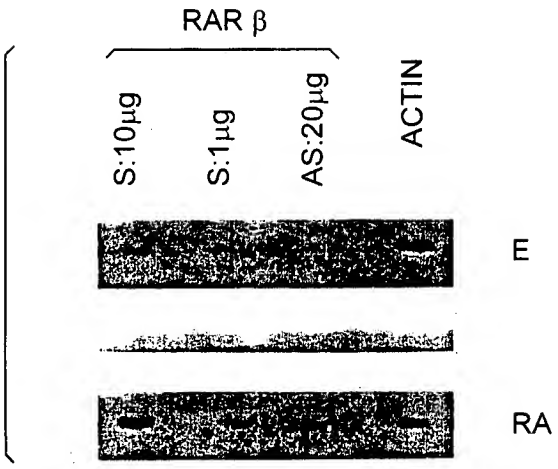
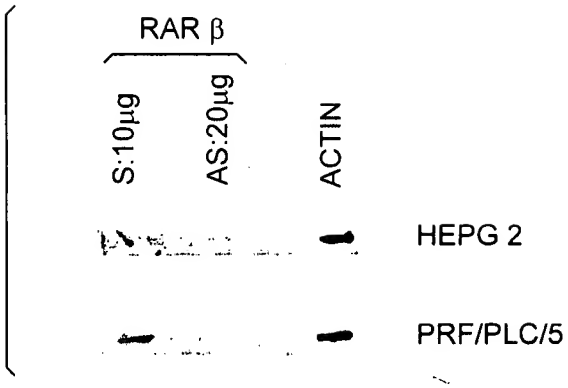


FIG. 13



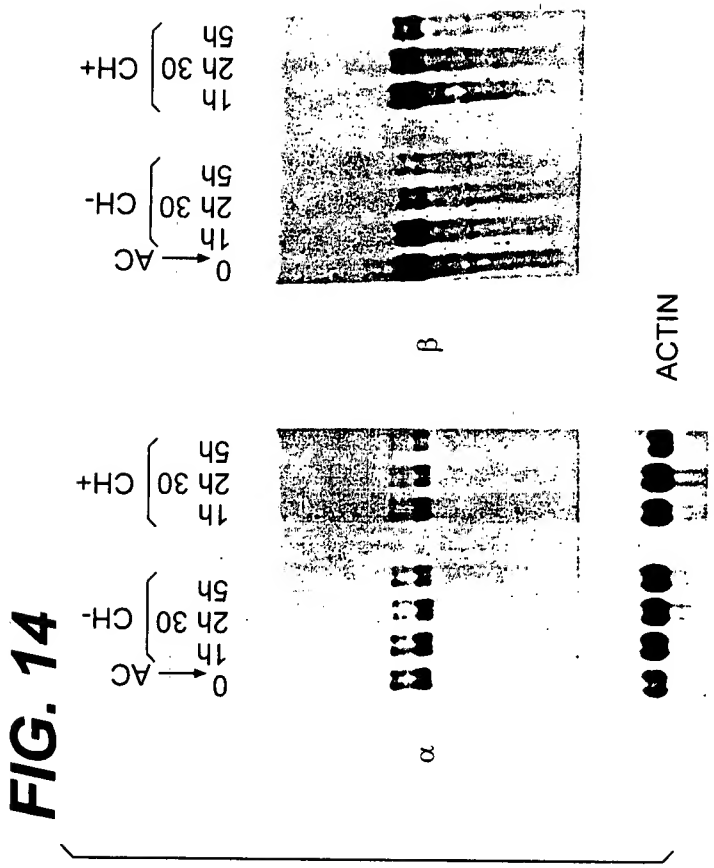


FIG. 14

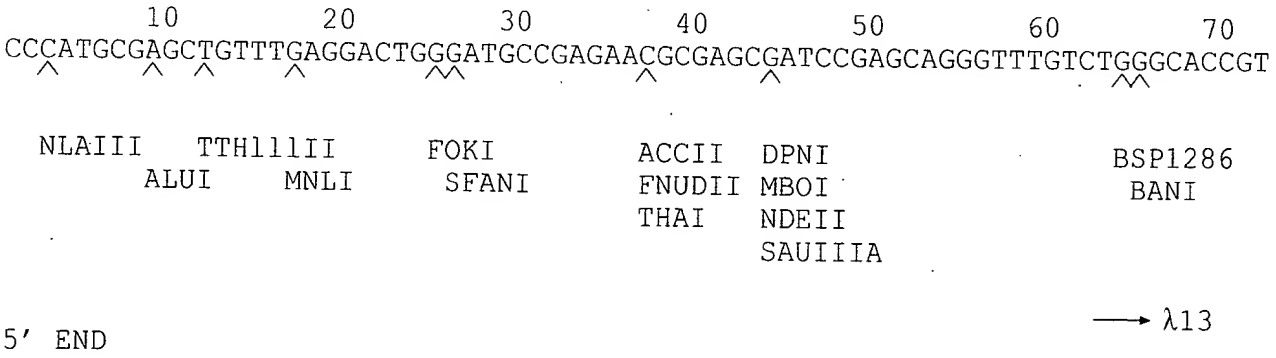


FIG. 15

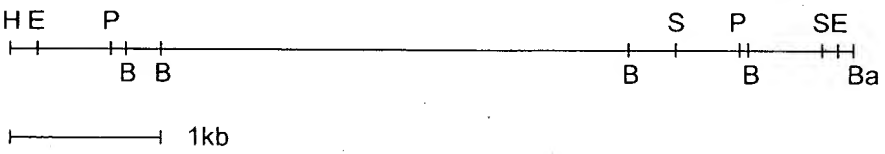


FIG. 16